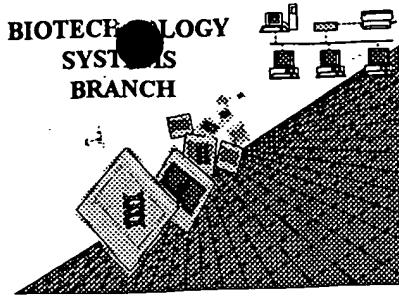


RAW SEQUENCE LISTING ERROR REPORT



The Biotechnology Systems Branch of the Scientific and Technical Information Center (STIC) detected errors when processing the following computer readable form:

Application Serial Number: 09/938,842

Source: OIPE

Date Processed by STIC: 9/13/2001

THE ATTACHED PRINTOUT EXPLAINS DETECTED ERRORS.

PLEASE FORWARD THIS INFORMATION TO THE APPLICANT BY EITHER:

- 1) **INCLUDING A COPY OF THIS PRINTOUT IN YOUR NEXT COMMUNICATION TO THE APPLICANT, WITH A NOTICE TO COMPLY or,**
- 2) **TELEPHONING APPLICANT AND FAXING A COPY OF THIS PRINTOUT, WITH A NOTICE TO COMPLY**

FOR CRF SUBMISSION QUESTIONS, PLEASE CONTACT MARK SPENCER, 703-308-4212.

FOR SEQUENCE RULES INTERPRETATION, PLEASE CONTACT ROBERT WAX, 703-308-4216.

PATENTIN 2.1 e-mail help: patin21help@uspto.gov or phone 703-306-4119 (R. Wax)

PATENTIN 3.0 e-mail help: patin3help@uspto.gov or phone 703-306-4119 (R. Wax)

TO REDUCE ERRORED SEQUENCE LISTINGS, PLEASE USE THE CHECKER VERSION 3.0 PROGRAM, ACCESSIBLE THROUGH THE U.S. PATENT AND TRADEMARK OFFICE WEBSITE. SEE BELOW:

Checker Version 3.0

The Checker Version 3.0 application is a state-of the-art Windows based software program employing a logical and intuitive user-interface to check whether a sequence listing is in compliance with format and content rules. Checker Version 3.0 works for sequence listings generated for the original version of 37 CFR §§1.821 – 1.825 effective October 1, 1990 (old rules) and the revised version (new rules) effective July 1, 1998 as well as World Intellectual Property Organization (WIPO) Standard ST.25.

Checker Version 3.0 replaces the previous DOS-based version of Checker, and is Y2K-compliant. Checker allows public users to check sequence listings in Computer Readable form (CRF) before submitting them to the United States Patent and Trademark Office (USPTO). Use of Checker prior to filing the sequence listing is expected to result in fewer errored sequence listings, thus saving time and money.

Checker Version 3.0 can be down loaded from the USPTO website at the following address:
<http://www.uspto.gov/web/offices/pac/checker>

OIPE

RAW SEQUENCE LISTING
PATENT APPLICATION: US/09/938,842

DATE: 09/13/2001
TIME: 16:32:16

Input Set : N:\paola\09938842.txt
Output Set: N:\CRF3\09132001\I938842.raw

Does Not Comply
Corrected Diskette Needed

1 <110> APPLICANT: Harper, Jeff
2 Kreps, Joel
3 Wang, Xun
4 Zhu, Tong
6 <120> TITLE OF INVENTION: STRESS-REGULATED GENES OF PLANTS, TRANSGENIC PLANTS
CONTAINING SAME, AND *methods*
7 METHODS OF USE
9 <130> FILE REFERENCE: SCRIP1300-3
DC 11 <140> CURRENT APPLICATION NUMBER: US/09/938,842
DC 11 <141> CURRENT FILING DATE: 2001-08-24
11 <150> PRIOR APPLICATION NUMBER: US 60/227,866
W--> 12 <151> PRIOR FILING DATE: *2000-8-24* 2000-08-24
14 <150> PRIOR APPLICATION NUMBER: US 60/264,647
W--> 15 <151> PRIOR FILING DATE: *2001-1-16* 2001-01-16
17 <150> PRIOR APPLICATION NUMBER: US 60/300,111
W--> 18 <151> PRIOR FILING DATE: *2001-6-22* 2001-06-22
20 <160> NUMBER OF SEQ ID NOS: 5379

ERRORED SEQUENCES

15509 <210> SEQ ID NO: 304
15510 <211> LENGTH: 421
15511 <212> TYPE: DNA
15512 <213> ORGANISM: Arabidopsis thaliana
15514 <220> FEATURE:
15515 <221> NAME/KEY: N_region
15516 <222> LOCATION: (3)..(3)
15517 <223> OTHER INFORMATION: n = any nucleotide
15519 <400> SEQUENCE: 304 *Slashes are invalid*

invalid use N and explain in 227-127

E--> 15520 *ncgi* tgg ctttcgagcg gcccgggg caggtaaacc acctttatta ccattcagg
E--> 15522 ttcaacat aggtgagatg atgacttgc gaagatata tcctgtata tccccaaagg
E--> 15524 tcattgaagg gcttaccctt gaagttcaa ttggcacgc agcgaaaaa ctggcgatt
E--> 15526 tgattagact tccaaactgtat gaacccgggt ttaaggcgg aatcagttgg ttgtctaaat
E--> 15528 ctgctttga ttcaattgtcttacttcaga gcaatctaacc caagtttg tctggttctt
E--> 15530 gatctccgtt tggtttgtt tggagattaa ttcgcttccg tatgaaagac aaatggggag
E--> 15532 tgtccctttg tatttttat tggatatcc ttgttataaaa aaaaaaaaaaaa aaaaaaaaaaaa
E--> 15534 a
89510 <210> SEQ ID NO: 1784
89511 <211> LENGTH: 467
89512 <212> TYPE: DNA
89513 <213> ORGANISM: Arabidopsis thaliana
89515 <220> FEATURE:
89516 <221> NAME/KEY: N_region
89517 <222> LOCATION: (3)..(3)
89518 <223> OTHER INFORMATION: n = any nucleotide
89520 <400> SEQUENCE: 1784
E--> 89521 *ncgi* att gggtttacag tttacttagac cagatgtggg ggggtttggg tacaaaagg

60
120
180
240
300
360
420
421

(60) 57 nos off

RAW SEQUENCE LISTING
PATENT APPLICATION: US/09/938,842

DATE: 09/13/2001
TIME: 16:32:24

Input Set : N:\paola\09938842.txt
Output Set: N:\CRF3\09132001\I938842.raw

E--> 89523 ccagactgg tttcgaaagg taaaatgga aaaactgatc agcaggcggg ataggacggg	120
E--> 89525 gctggccac aggtacagc ctacagttt atcatacata cctaaacctt ataatcagg	180
E--> 89527 taggcagata tagtagcctt acaagttaga actatctcaa ttccataagtc ccaagtccct	240
E--> 89529 aagccctcct ttgccatggc tcttttgaa acttagcactt taagataatc gcattttctc	300
E--> 89531 tcatctcctt gggctctca caaaactaaat ttgtgggca acttcaatct tggtttctag	360
E--> 89533 tatatgtgca aagatattaa aatcagttaa aaatttagttt gtgttagtat ttggagttta	420
E--> 89535 taaaattttaaa aatatctact acttcaatca aaagtcgacg cgccgc	467
123106 <210> SEQ ID NO: 2469	
123107 <211> LENGTH: 245	
123108 <212> TYPE: DNA	
123109 <213> ORGANISM: Arabidopsis thaliana	
123111 <220> FEATURE:	
123112 <221> NAME/KEY: N_region	
123113 <222> LOCATION: (3)..(3)	
123114 <223> OTHER INFORMATION: n = any nucleotide <i>same error</i>	
123116 <400> SEQUENCE: 2469	
E--> 123117 (ncg) tcg agcggccgccc cggcaggta ccaaaccgga aaatacagtc tcataactttt	
E--> 123119 aagtttttct gtttcagat aagagatgac tgctttctt ccttttgtt aggaaaccat	
E--> 123121 cttctccact taatttccat aattttcttg ctttgttaga gttacgactc cacttttttg	
E--> 123123 cttcttgtaa tgtttctcta tttaaaaaaaa accaaaaaaaaaaa aaaaaaaaaaaa aaaaaaaaaaaa	
E--> 123125 aaaaa	

h05.
J off

OS? 60
120
180
240
245

Use of n and/or Xaa has been detected in the Sequence Listing.

→ Review the Sequence Listing to insure a corresponding explanation is presented in the <220> to <223> fields of each sequence using n or Xaa.

VERIFICATION SUMMARY
PATENT APPLICATION: US/09/938,842

DATE: 09/13/2001
TIME: 16:32:49

Input Set : N:\paola\09938842.txt
Output Set: N:\CRF3\09132001\I938842.raw

L:11 M:270 C: Current Application Number differs, Replaced Current Application No
L:11 M:271 C: Current Filing Date differs, Replaced Current Filing Date
L:12 M:256 W: Invalid Numeric Header Field, Wrong Prior FILING DATE:YYYY-MM-DD
L:15 M:256 W: Invalid Numeric Header Field, Wrong Prior FILING DATE:YYYY-MM-DD
L:18 M:256 W: Invalid Numeric Header Field, Wrong Prior FILING DATE:YYYY-MM-DD
L:15520 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:304
L:15520 M:254 E: No. of Bases conflict, LENGTH:Input:60 Counted:58 SEQ:304
L:15520 M:320 E: (1) Wrong Nucleic Acid Designator, NUMBER OF INVALID KEYS:2
M:254 Repeated in SeqNo=304
L:15534 M:252 E: No. of Seq. differs, <211>LENGTH:Input:421 Found:419 SEQ:304
L:89521 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:1784
L:89521 M:254 E: No. of Bases conflict, LENGTH:Input:60 Counted:58 SEQ:1784
L:89521 M:320 E: (1) Wrong Nucleic Acid Designator, NUMBER OF INVALID KEYS:2
M:254 Repeated in SeqNo=1784
L:89535 M:252 E: No. of Seq. differs, <211>LENGTH:Input:467 Found:465 SEQ:1784
L:123117 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:2469
L:123117 M:254 E: No. of Bases conflict, LENGTH:Input:60 Counted:58 SEQ:2469
L:123117 M:320 E: (1) Wrong Nucleic Acid Designator, NUMBER OF INVALID KEYS:2
M:254 Repeated in SeqNo=2469
L:123125 M:252 E: No. of Seq. differs, <211>LENGTH:Input:245 Found:243 SEQ:2469
L:179888 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:3467
L:205509 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:3913